



PCT10

ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,919A

DATE: 07/24/2002

TIME: 11:53:40

Input Set : A:\DAVI151SEQLIST.TXT

Output Set: N:\CRF3\07242002\J009919A.raw

4 <110> APPLICANT: Panaccio, Michael
 5 Rosey, Everett Lee
 6 Hasse, Detlef
 7 Ankenbauer, Robert G.
 9 <120> TITLE OF INVENTION: LAWSONIA DERIVED GENE AND RELATED
 10 HEMOLYSIN POLYPEPTIDES, PEPTIDES AND PROTEINS AND THEIR USES
 13 <130> FILE REFERENCE: DAVI151.001APC
 15 <140> CURRENT APPLICATION NUMBER: US 10/009,919A
 C--> 16 <141> CURRENT FILING DATE: 2002-06-14
 18 <150> PRIOR APPLICATION NUMBER: PCT/AU00/00439
 19 <151> PRIOR FILING DATE: 2000-05-11
 21 <150> PRIOR APPLICATION NUMBER: US 60/134,022
 22 <151> PRIOR FILING DATE: 1999-05-13
 24 <160> NUMBER OF SEQ ID NOS: 11
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 251
 30 <212> TYPE: PRT
 31 <213> ORGANISM: Lawsonia intracellularis
 33 <400> SEQUENCE: 1
 34 Met Ala Lys His Lys Val Arg Ala Asp Glu Leu Val Phe Leu Gln Gly
 35 1 5 10 15
 36 Leu Ala Glu Ser Arg Glu Gln Ala Lys Arg Leu Ile Met Ala Gly Lys
 37 20 25 30
 38 Val Thr Leu Thr Asn Asn Ser Thr Thr Ile Pro Leu Arg Leu Glu Lys
 39 35 40 45
 40 Pro Gly His Lys Tyr Pro Leu Glu Ser Ile Cys Ser Leu Ile Gly Val
 41 50 55 60
 42 Glu Arg Phe Val Ser Arg Gly Ala Tyr Lys Leu Leu Thr Ala Leu Asp
 43 65 70 75 80
 44 Phe Phe Lys Ile Asp Val Lys Ser Cys Ile Cys Leu Asp Ala Gly Ala
 45 85 90 95
 46 Ser Thr Gly Gly Phe Thr Asp Cys Leu Leu Gln His Gly Ala Ser Lys
 47 100 105 110
 48 Val Tyr Ala Ile Asp Val Gly Lys Gly Gln Leu His Glu Lys Leu Tyr
 49 115 120 125
 50 Thr Asn Glu Gln Val Ile Asn Ile Glu Gly Val Asn Leu Arg Thr Ala
 51 130 135 140
 52 Ser Lys Asp Leu Ile Pro Glu Glu Val Asp Ile Leu Thr Ile Asp Val
 53 145 150 155 160
 54 Ser Phe Ile Ser Leu Thr Leu Ile Leu Pro Ser Cys Ile Arg Trp Leu
 55 165 170 175
 56 Lys Ala Ser Gly Ile Ile Ile Ala Leu Ile Lys Pro Gln Phe Glu Leu

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57          180          185          190
58 Tyr Pro Asp Lys Ile Lys Lys Gly Val Val Lys Glu Thr Ser Leu Gln
59          195          200          205
60 Tyr Glu Ala Val Glu Lys Ile Ile His Phe Cys Gln Ser Glu Leu Gly
61          210          215          220
62 Leu Ile Phe Ile Gly Val Val Pro Ser Val Ile Lys Gly Pro Lys Gly
63 225          230          235          240
64 Asn Gln Glu Tyr Leu Ile Tyr Leu Lys Lys Arg
65          245          250
68 <210> SEQ ID NO: 2
69 <211> LENGTH: 756
70 <212> TYPE: DNA
71 <213> ORGANISM: Lawsonia intracellularis
73 <220> FEATURE:
74 <221> NAME/KEY: CDS
75 <222> LOCATION: (1)...(756)
77 <400> SEQUENCE: 2
78 atg gcc aaa cat aaa gta cgt gct gat gaa ctt gtt ttt tta caa ggg 48
79 Met Ala Lys His Lys Val Arg Ala Asp Glu Leu Val Phe Leu Gln Gly
80 1          5          10          15
82 tta gca gaa agt cgt gaa caa gct aaa cga ctt att atg gca ggt aag 96
83 Leu Ala Glu Ser Arg Glu Gln Ala Lys Arg Leu Ile Met Ala Gly Lys
84          20          25          30
86 gtt aca tta act aat aat tct aca act ata cca tta cgt ttg gaa aaa 144
87 Val Thr Leu Thr Asn Asn Ser Thr Thr Ile Pro Leu Arg Leu Glu Lys
88          35          40          45
90 cca gga cat aaa tat cca tta gaa agt atc tgc agt tta ata ggg gta 192
91 Pro Gly His Lys Tyr Pro Leu Glu Ser Ile Cys Ser Leu Ile Gly Val
92          50          55          60
94 gaa cgt ttt gtg agt aga gga gca tat aag cta tta act gct cta gat 240
95 Glu Arg Phe Val Ser Arg Gly Ala Tyr Lys Leu Leu Thr Ala Leu Asp
96 65          70          75          80
98 ttt ttt aaa att gat gta aaa agt tgt att tgt ctt gat gca ggc gca 288
99 Phe Phe Lys Ile Asp Val Lys Ser Cys Ile Cys Leu Asp Ala Gly Ala
100          85          90          95
102 tct act ggt ggg ttt aca gat tgt ctt tta caa cat gga gca tct aaa 336
103 Ser Thr Gly Gly Phe Thr Asp Cys Leu Leu Gln His Gly Ala Ser Lys
104          100          105          110
106 gta tat gcg att gat gta ggc aaa ggt caa tta cat gag aaa ctg tat 384
107 Val Tyr Ala Ile Asp Val Gly Lys Gly Gln Leu His Glu Lys Leu Tyr
108          115          120          125
110 act aat gaa caa gtt ata aat att gag gga gtg aat tta cgt aca gca 432
111 Thr Asn Glu Gln Val Ile Asn Ile Glu Gly Val Asn Leu Arg Thr Ala
112          130          135          140
114 tct aaa gat ctt att cct gaa gaa gta gat att tta act att gat gtt 480
115 Ser Lys Asp Leu Ile Pro Glu Glu Val Asp Ile Leu Thr Ile Asp Val
116 145          150          155          160
118 tct ttt ata tcg ctt act ttg att tta ccg tca tgt ata cgt tgg cta 528
119 Ser Phe Ile Ser Leu Thr Leu Ile Leu Pro Ser Cys Ile Arg Trp Leu

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120                               165                               170                               175
122 aag gct tcc gga att att att gcc tta ata aag cct caa ttt gaa tta 576
123 Lys Ala Ser Gly Ile Ile Ile Ala Leu Ile Lys Pro Gln Phe Glu Leu
124                               180                               185                               190
126 tat cca gat aaa ata aaa aaa ggt gta gta aaa gaa act agc ttg caa 624
127 Tyr Pro Asp Lys Ile Lys Lys Gly Val Val Lys Glu Thr Ser Leu Gln
128                               195                               200                               205
130 tat gaa gca gta gaa aaa att att cat ttt tgt caa tca gaa ctt gga 672
131 Tyr Glu Ala Val Glu Lys Ile Ile His Phe Cys Gln Ser Glu Leu Gly
132                               210                               215                               220
134 ctt ata ttt att ggt gtt gtt ccg tcg gta ata aaa ggt cca aaa gga 720
135 Leu Ile Phe Ile Gly Val Val Pro Ser Val Ile Lys Gly Pro Lys Gly
136 225                               230                               235                               240
138 aat caa gaa tat ctt att tac ttg aaa aaa cgt taa 756
139 Asn Gln Glu Tyr Leu Ile Tyr Leu Lys Lys Arg *
140                               245                               250
143 <210> SEQ ID NO: 3
144 <211> LENGTH: 15
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
148 <220> FEATURE:
149 <223> OTHER INFORMATION: Oligonucleotide primer RA168.
151 <400> SEQUENCE: 3
152 aaataataag atgag 15
154 <210> SEQ ID NO: 4
155 <211> LENGTH: 22
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Oligonucleotide primer RA169.
162 <400> SEQUENCE: 4
163 atagaataca aattataata ag 22
165 <210> SEQ ID NO: 5
166 <211> LENGTH: 240
167 <212> TYPE: PRT
168 <213> ORGANISM: Serpulina (Treponema) hyodysenteriae
170 <400> SEQUENCE: 5
171 Met Arg Leu Asp Glu Tyr Val His Ser Glu Glu Val Val Gln Asn Ile
172 1 5 10 15
173 Lys Tyr Val Ser Arg Ala Gly Glu Gly Tyr Thr Glu Ser Arg Ser Lys
174 20 25 30
175 Ala Gln Asp Ile Ile Leu Ala Gly Cys Val Phe Val Asn Gly Lys Leu
176 35 40 45
177 Glu Lys Ala Phe Val Glu Phe Gly Ile Ser Val Glu Asn Lys Ile Cys
178 50 55 60
179 Leu Asp Ile Gly Val Lys Val Thr Ser Lys Ala His Lys Ile Lys Asp
180 65 70 75 80
181 Thr Asp Asn Ile Ala Ser Thr Gly Gly Phe Thr Asp Cys Leu Leu Lys
182 85 90 95

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183 His Gly Ala Lys Lys Val Tyr Ala Leu Asp Val Gly His Asn Gln Leu
184          100          105          110
185 Val Tyr Lys Leu Arg Asn Asp Asn Arg Val Glu Leu Asn Asn Leu Glu
186          115          120          125
187 Phe Trp Val Thr Leu Ile Lys Pro Gln Phe Val Ser Ile Glu Asp Phe
188          130          135          140
189 Asn Ala Lys Asp Ile Asn Lys Glu Met Phe Asn Asp Glu Ile Glu Ala
190 145          150          155          160
191 Glu Arg Gly Asp Val Ser Lys Gly Gly Ile Ile Arg Asp Asp Ile Leu
192          165          170          175
193 Arg Pro Ser Val Ile Val Ser Asp Val Ser Phe Ile Ser Ile Thr Lys
194          180          185          190
195 Ile Ala Pro Ile Ile Phe Lys Glu Lys Ile Leu Asn Asn Ala Ile Ser
196          195          200          205
197 Lys Ile Ile Asp Cys Gly Phe Lys Glu Val Asn Arg Thr Ile Ser Pro
198          210          215          220
199 Ile Lys Gly Ala Lys Gly Asn Ile Glu Tyr Leu Ala His Phe Ile Ile
200 225          230          235          240
203 <210> SEQ ID NO: 6
204 <211> LENGTH: 268
205 <212> TYPE: PRT
206 <213> ORGANISM: Mycobacterium tuberculosis
208 <400> SEQUENCE: 6
209 Met Ala Arg Arg Ala Arg Val Asp Ala Glu Leu Val Arg Arg Thr Val
210 1          5          10          15
211 Val Thr Asp Ser Glu Arg Ala Trp Val Ser Arg Gly Ala His Gly Leu
212          20          25          30
213 Ala Arg Ser Arg Gln Gln Ala Ala Glu Leu Ile Gly Ala Gly Lys Val
214          35          40          45
215 Arg Ile Asp Gly Lys Leu Val Gly Ala Leu Glu Ala Phe Ala Ile Ala
216          50          55          60
217 Val Ala Gly Arg Arg Cys Leu Asp Ala Gly Leu Pro Ala Val Lys Pro
218 65          70          75          80
219 Ala Thr Ala Val Ser Asp Thr Thr Ala Leu Ala Ser Thr Gly Gly Phe
220          85          90          95
221 Thr Glu Val Leu Leu Asp Arg Gly Ala Ala His Val Val Ala Ala Asp
222          100          105          110
223 Val Gly Tyr Gly Gln Leu Ala Trp Ser Leu Arg Asn Asp Pro Arg Val
224          115          120          125
225 Cys Ala Ser Arg Asp Ala Asp Ile Val Pro Leu Val Lys Pro Gln Phe
226          130          135          140
227 Val Val Leu Glu Arg Thr Asn Ala Arg Gly Leu Thr Pro Glu Ala Ile
228 145          150          155          160
229 Gly Gly Arg Glu Val Gly Lys Gly Gln Val Gly Pro Gly Gly Val Val
230          165          170          175
231 His Asp Pro Gln Leu Arg Val Asp Leu Val Val Ala Asp Leu Ser Phe
232          180          185          190
233 Ile Ser Leu Ala Thr Val Leu Pro Ala Leu Val Gly Ala Arg Ser Val
234          195          200          205

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235 Leu Ala Val Ala Arg Arg Ala Gln Glu Leu Gly Trp His Ser Val Gly
236      210                      215                      220
237 Val Lys Ala Ser Pro Leu Pro Gly Pro Ser Gly Asn Val Glu Tyr Phe
238 225                      230                      235                      240
239 Leu Trp Leu Arg Thr Gln Thr Asp Arg Ala Leu Ser Ala Lys Gly Leu
240                      245                      250                      255
241 Glu Asp Ala Val His Arg Ala Ile Ser Glu Gly Pro
242      260                      265
245 <210> SEQ ID NO: 7
246 <211> LENGTH: 258
247 <212> TYPE: PRT
248 <213> ORGANISM: Aquifex aeolicus
250 <400> SEQUENCE: 7
251 Met Arg Leu Asp Lys Tyr Leu Thr Asp Lys Glu Val Lys Glu Leu Pro
252 1                      5                      10                      15
253 Lys Tyr Val Ser Arg Gly Gly Glu Gly Ile Val Pro Ser Arg Glu Lys
254      20                      25                      30
255 Ala Gln Ala Val Ile Met Ala Gly Gln Val Leu Val Asn Gly Lys Leu
256      35                      40                      45
257 Glu Trp Ala Ile Lys Arg Phe Ser Leu Asp Leu Lys Asp Lys Val Val
258      50                      55                      60
259 Leu Asp Val Gly Lys Val Val Asp Lys Pro Gly Tyr Arg Leu Lys Gly
260 65                      70                      75                      80
261 Asn Glu Lys Val Ser Ser Thr Gly Gly Phe Thr Asp Cys Ala Leu Gln
262      85                      90                      95
263 His Gly Ala Lys Lys Val Tyr Ala Val Asp Val Gly Arg Gly Gln Met
264      100                     105                     110
265 Asp Tyr Lys Leu Arg Gln Asp Pro Pro Val Phe Leu Lys Glu Asp Gly
266      115                     120                     125
267 Leu Leu Leu Val Leu Val Lys Pro Gln Phe Val Leu Tyr Glu Glu Thr
268      130                     135                     140
269 Asp Ala Arg Glu Leu Ser Glu Glu His Val Pro Glu Lys Glu Leu Cys
270 145                     150                     155                     160
271 Pro Arg Lys Val Lys Lys Gly Val Val Arg Glu Lys Glu His Lys Val
272      165                     170                     175
273 Asp Leu Ile Thr Cys Asp Val Ser Phe Ile Ser Ser Thr Lys Val Leu
274      180                     185                     190
275 Pro Asn Val Phe Lys Arg Glu Ala Leu Gln Lys Val Val Asn Phe Leu
276      195                     200                     205
277 Lys Glu Asn Gly Phe Arg Ile Leu Gly Val Ile Lys Ser Lys Pro Lys
278      210                     215                     220
279 Gly Thr Lys Gly Asn Glu Phe Phe Val Leu Ala Gly Arg Lys Gly
280 225                     230                     235                     240
281 Glu Glu Val Asn Leu Ser Glu Ala Ile Glu Lys Ala Leu Glu Glu Val
282      245                     250                     255
283 Val Asp
287 <210> SEQ ID NO: 8
288 <211> LENGTH: 262
289 <212> TYPE: PRT

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VERIFICATION SUMMARY

DATE: 7/24/2002

PATENT APPLICATION: US/10/009,919A

TIME: 11:53:41

Input Set : A:\DAVI151SEQLIST.TXT

Output Set: N:\CRF3\07242002\J009919A.raw

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date